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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/856,050

DATE: 10/11/2001
TIME: 09:50:56

Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\10112001\I856050.raw

3 <110> APPLICANT: UEMURA, Hidetoshi
4 OKUI, Akira
5 KOMINAMI, Katsuya
6 YAMAGUCHI, Nozomi
7 MITSUI, Shinichi
9 <120> TITLE OF INVENTION: PROTEIN EXPRESSION VECTOR AND USE THEREOF
11 <130> FILE REFERENCE: UEMURA=8
13 <140> CURRENT APPLICATION NUMBER: 09/856,050
14 <141> CURRENT FILING DATE: 2001-05-17
16 <150> PRIOR APPLICATION NUMBER: JP 10/331515
17 <151> PRIOR FILING DATE: 1998-11-20
19 <150> PRIOR APPLICATION NUMBER: PCT/JP99/06474
20 <151> PRIOR FILING DATE: 1999-11-19
22 <160> NUMBER OF SEQ ID NOS: 22
24 <170> SOFTWARE: PatentIn version 3.1
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29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Synthetic ✓
34 <220> FEATURE:
35 <221> NAME/KEY: misc_feature
36 <223> OTHER INFORMATION: Designed oligonucleotide to construct plasmid pTrypHis
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69 <220> FEATURE:
70 <223> OTHER INFORMATION: Synthetic ✓
72 <220> FEATURE:
73 <221> NAME/KEY: misc_feature

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74 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify neurosin-encoding
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 78 <400> SEQUENCE: 3
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 84 <212> TYPE: DNA
 85 <213> ORGANISM: Artificial Sequence
 87 <220> FEATURE:
 88 <223> OTHER INFORMATION: Synthetic ✓
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 114 <400> SEQUENCE: 5
 115 ctaagcttga cgacgatgac aagttg 26
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 120 <212> TYPE: DNA
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 127 tcctcgagac ttggcctgaa tggtttt 27
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 132 <212> TYPE: DNA
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 139 <221> NAME/KEY: misc_feature
 140 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify a portion of
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 144 <400> SEQUENCE: 7
 145 ccaagcttca ccatcaccat caccat 26
 148 <210> SEQ ID NO: 8

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Input Set : A:\sequence listing.txt

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 158 <223> OTHER INFORMATION: Designed oligonucleotide to construct plasmid pSecTrypHis
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 164 tgctgcccccc tttgacgacg atgacaaggaa tccgaattc 99
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 172 <220> FEATURE:
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 175 <220> FEATURE:
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 177 <223> OTHER INFORMATION: Designed oligonucleotide to construct plasmid pSecTrypHis
 180 <400> SEQUENCE: 9
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 189 <213> ORGANISM: Artificial Sequence
 191 <220> FEATURE:
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 194 <220> FEATURE:
 195 <221> NAME/KEY: misc_feature
 196 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify a portion of plasmid p
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 205 <211> LENGTH: 29
 206 <212> TYPE: DNA
 207 <213> ORGANISM: Artificial Sequence
 209 <220> FEATURE:
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 212 <220> FEATURE:
 213 <221> NAME/KEY: misc_feature
 214 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify a portion of plasmid p
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 218 <400> SEQUENCE: 11
 219 tgaagcttgc catggccaa cttgtcatc 29
 222 <210> SEQ ID NO: 12
 223 <211> LENGTH: 17

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Input Set : A:\sequence listing.txt
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 232 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify a portion of
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 237 gcacagtcga ggctgat 17
 240 <210> SEQ ID NO: 13
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 243 <213> ORGANISM: Artificial Sequence
 245 <220> FEATURE:
 246 <223> OTHER INFORMATION: Synthetic *OV*
 248 <220> FEATURE:
 249 <221> NAME/KEY: misc_feature
 250 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify a portion of
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 255 caaatgtggat atggctg 17
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 259 <211> LENGTH: 672
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 261 <213> ORGANISM: Homo sapiens
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 264 <221> NAME/KEY: CDS
 265 <222> LOCATION: (1)..(672)
 266 <223> OTHER INFORMATION:
 269 <400> SEQUENCE: 14
 270 ttg gtg cat ggc gga ccc tgc gac aag aca tct cac ccc tac caa gct 48
 271 Leu Val His Gly Gly Pro Cys Asp Lys Thr Ser His Pro Tyr Gln Ala
 272 1 5 10 15
 274 gcc ctc tac acc tcg ggc cac ttg ctc tgt ggt ggg gtc ctt atc cat 96
 275 Ala Leu Tyr Thr Ser Gly His Leu Leu Cys Gly Val Leu Ile His
 276 20 25 30
 278 cca ctg tgg gtc ctc aca gct gcc cac tgc aaa aaa ccg aat ctt cag 144
 279 Pro Leu Trp Val Leu Thr Ala Ala His Cys Lys Lys Pro Asn Leu Gln
 280 35 40 45
 282 gtc ttc ctg ggg aag cat aac ctt cgg caa agg gag agt tcc cag gag 192
 283 Val Phe Leu Gly Lys His Asn Leu Arg Gln Arg Glu Ser Ser Gln Glu
 284 50 55 60
 286 cag agt tct gtt gtc cgg gct gtg atc cac cct gac tat gat gcc gcc 240
 287 Gln Ser Ser Val Val Arg Ala Val Ile His Pro Asp Tyr Asp Ala Ala
 288 65 70 75 80
 290 agc cat gac cag gac atc atg ctg ttg cgc ctg gca cgc cca gcc aaa 288
 291 Ser His Asp Gln Asp Ile Met Leu Leu Arg Leu Ala Arg Pro Ala Lys
 292 85 90 95

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294	ctc	tct	gaa	ctc	atc	cag	ccc	ctt	ccc	ctg	gag	agg	gac	tgc	tca	gcc	336
295	Leu	Ser	Glu	Leu	Ile	Gln	Pro	Leu	Pro	Leu	Glu	Arg	Asp	Cys	Ser	Ala	
296				100					105					110			
298	aac	acc	acc	agc	tgc	cac	atc	ctg	ggc	tgg	ggc	aag	aca	gca	gat	ggt	384
299	Asn	Thr	Thr	Ser	Cys	His	Ile	Leu	Gly	Trp	Gly	Lys	Thr	Ala	Asp	Gly	
300					115			120				125					
302	gat	ttc	cct	gac	acc	atc	cag	tgt	gca	tac	atc	cac	ctg	gtg	tcc	cgt	432
303	Asp	Phe	Pro	Asp	Thr	Ile	Gln	Cys	Ala	Tyr	Ile	His	Leu	Val	Ser	Arg	
304					130			135				140					
306	gag	gag	tgt	gag	cat	gcc	tac	cct	ggc	cag	atc	acc	cag	aac	atg	ttg	480
307	Glu	Glu	Cys	Glu	His	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Gln	Asn	Met	Leu	
308					145			150			155			160			
310	tgt	gct	ggg	gat	gag	aag	tac	ggg	aag	gat	tcc	tgc	cag	ggt	gat	tct	528
311	Cys	Ala	Gly	Asp	Glu	Lys	Tyr	Gly	Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	
312					165			170			175						
314	ggg	ggt	ccg	ctg	gta	tgt	gga	gac	cac	ctc	cga	ggc	ctt	gtg	tca	tgg	576
315	Gly	Gly	Pro	Leu	Val	Cys	Gly	Asp	His	Leu	Arg	Gly	Leu	Val	Ser	Trp	
316					180			185			190						
318	ggt	aat	atc	ccc	tgt	gga	tca	aag	gag	aag	cca	gga	gtc	tac	acc	aac	624
319	Gly	Asn	Ile	Pro	Cys	Gly	Ser	Lys	Glu	Lys	Pro	Gly	Val	Tyr	Thr	Asn	
320					195			200			205						
322	gtc	tgc	aga	tac	acg	aac	tgg	atc	caa	aaa	acc	att	cag	gcc	aag	tga	672
323	Val	Cys	Arg	Tyr	Thr	Asn	Trp	Ile	Gln	Lys	Thr	Ile	Gln	Ala	Lys		
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330	<213> ORGANISM: Homo sapiens																
332	<220> FEATURE:																
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338	1				5				10				15				
341	Ala	Leu	Tyr	Thr	Ser	Gly	His	Leu	Leu	Cys	Gly	Val	Leu	Ile	His		
342					20				25			30					
345	Pro	Leu	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys	Lys	Pro	Asn	Leu	Gln	
346					35			40			45						
349	Val	Phe	Leu	Gly	Lys	His	Asn	Leu	Arg	Gln	Arg	Glu	Ser	Ser	Gln	Glu	
350					50			55			60						
353	Gln	Ser	Ser	Val	Val	Arg	Ala	Val	Ile	His	Pro	Asp	Tyr	Asp	Ala	Ala	
354					65			70			75			80			
357	Ser	His	Asp	Gln	Asp	Ile	Met	Leu	Leu	Arg	Leu	Ala	Arg	Pro	Ala	Lys	
358					85			90			95						
361	Leu	Ser	Glu	Leu	Ile	Gln	Pro	Leu	Pro	Leu	Glu	Arg	Asp	Cys	Ser	Ala	
362					100			105			110						
365	Asn	Thr	Thr	Ser	Cys	His	Ile	Leu	Gly	Trp	Gly	Lys	Thr	Ala	Asp	Gly	
366					115			120			125						
369	Asp	Phe	Pro	Asp	Thr	Ile	Gln	Cys	Ala	Tyr	Ile	His	Leu	Val	Ser	Arg	
370					130			135			140						

VERIFICATION SUMMARY

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